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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/039,659

DATE: 02/08/2002
TIME: 08:32:59

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Input Set : N:\Crf3\RULE60\10039659.txt
Output Set: N:\CRF3\02082002\J039659.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Wang, Wei
6 Gish, Kurt C.
7 Schall, Thomas J.
8 Vicari, Alain P.
9 Zlotnik, Albert
10
11 (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
12
13 (iii) NUMBER OF SEQUENCES: 19
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: DNAX Research Institute
17 (B) STREET: 901 California Avenue
18 (C) CITY: Palo Alto
19 (D) STATE: California
20 (E) COUNTRY: USA
21 (F) ZIP: 94304-1104
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US/10/039,659
C--> 31 (B) FILING DATE: 03-Jan-2002
C--> 32 (C) CLASSIFICATION:
33
34 C--> 44 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/887,977
36 (B) FILING DATE: 03-JUL-1997
37 (A) APPLICATION NUMBER: US 60/021,644
38 (B) FILING DATE: 05-JUL-1996
39 (A) APPLICATION NUMBER: US 60/028,329
40 (B) FILING DATE: 11-OCT-1996
41
42 (viii) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: Ching, Edwin P.
44 (B) REGISTRATION NUMBER: 34,090
45 (C) REFERENCE/DOCKET NUMBER: DX0589K1
46
47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: 650-852-9192
49 (B) TELEFAX: 650-496-1200
50
51 (2) INFORMATION FOR SEQ ID NO: 1:
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 1034 base pairs
54 (B) TYPE: nucleic acid

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63 (C) STRANDEDNESS: single
 64 (D) TOPOLOGY: linear
 66 (ii) MOLECULE TYPE: cDNA
 69 (ix) FEATURE:
 70 (A) NAME/KEY: CDS
 71 (B) LOCATION: 94..525
 74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 76 AGGCTACAAG CAGGCACCAAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT 60
 78 TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC 114
 79 Met Lys Leu Trp Leu Phe Ala
 80 1 5
 82 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC 162
 83 Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
 84 10 15 20
 86 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA 210
 87 Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
 88 25 30 35
 90 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT 258
 91 Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
 92 40 45 50 55
 94 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA 306
 95 Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
 96 60 65 70
 98 GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC 354
 99 Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
 100 75 80 85
 102 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT 402
 103 Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
 104 90 95 100
 106 CAG ACT GAA AGG AAG AAC TCA AAC CAT ATG AAG TCC AAG GTG GAG AAC 450
 107 Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn
 108 105 110 115
 110 CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG 498
 111 Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met
 112 120 125 130 135
 114 GTG ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA 545
 115 Val Met Met Pro Arg Lys Thr Asn Asn
 116 140
 118 AGCACCGAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC 605
 120 CAATGAACTC ACTGAAGCTA CAGTTCTCTG TACAAGACCA GACCCACCAA CGTCTCAGCA 665
 122 TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCACT CACCAAGGAG CTATTGGCTA 725
 124 TTGATGATTG CTGAGGAAG GGAGTAATT TTTTCTCTT TCTGAAGTGT GACTTGAGTA 785
 126 AATTGCCAT AGTTCACTATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA 845
 128 ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTAG 905
 130 GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGT AGAGTGCCTG 965
 132 CACGTGTGAA ATGGTCAAAG ATTAAAAAA TAAAAACTTA AAAAGCTATT AAAAAGTAAA 1025
 134 AAAATAAA 1034

137 (2) INFORMATION FOR SEQ ID NO: 2:

139 (i) SEQUENCE CHARACTERISTICS:

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Input Set : N:\Crf3\RULE60\10039659.txt
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140 (A) LENGTH: 144 amino acids
 141 (B) TYPE: amino acid
 142 (D) TOPOLOGY: linear
 144 (ii) MOLECULE TYPE: protein
 146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 148 Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala
 149 1 5 10 15
 151 Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu
 152 20 25 30
 154 Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn
 155 35 40 45
 157 Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg
 158 50 55 60
 160 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
 161 65 70 75 80
 163 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
 164 85 90 95
 166 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
 167 100 105 110
 169 Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
 170 115 120 125
 172 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
 173 130 135 140
 176 (2) INFORMATION FOR SEQ ID NO: 3:
 178 (i) SEQUENCE CHARACTERISTICS:
 179 (A) LENGTH: 1012 base pairs
 180 (B) TYPE: nucleic acid
 181 (C) STRANDEDNESS: single
 182 (D) TOPOLOGY: linear
 184 (ii) MOLECULE TYPE: cDNA
 187 (ix) FEATURE:
 188 (A) NAME/KEY: CDS
 189 (B) LOCATION: 117..566
 191 (ix) FEATURE:
 192 (A) NAME/KEY: mat_peptide
 193 (B) LOCATION: 186..566
 196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 198 TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCCGGCAT CAGCTCCCTT GACCCAGTGG 60
 200 ATATCGGTGG CCCCGTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116
 202 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
 203 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
 204 -23 -20 -15 -10
 206 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
 207 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
 208 -5 1 5
 210 GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260
 211 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
 212 10 15 20 25
 214 TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA 308

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| | | | | |
|-----|---|------|-----|-----|
| 215 | Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile | | | |
| 216 | 30 | 35 | 40 | |
| 218 | TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC | 356 | | |
| 219 | Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser | | | |
| 220 | 45 | 50 | 55 | |
| 222 | AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT | 404 | | |
| 223 | Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val | | | |
| 224 | 60 | 65 | 70 | |
| 226 | TTT GCA AAG CTC CAC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT | 452 | | |
| 227 | Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His | | | |
| 228 | 75 | 80 | 85 | |
| 230 | GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG | 500 | | |
| 231 | Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys | | | |
| 232 | 90 | 95 | 100 | 105 |
| 234 | TTT AGC AAT CCC ATC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA | 548 | | |
| 235 | Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile | | | |
| 236 | 110 | 115 | 120 | |
| 238 | TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTCTGGG CTCCATCGGC | 596 | | |
| 239 | Ser Ala Asn Ser Gly Leu | | | |
| 240 | 125 | | | |
| 242 | ACAGGAGGGG CGGGATCTTT CTCCGATAAAA ACCGTCGCC TACAGACCCA GCTGTCCCCA | 656 | | |
| 244 | CGCCTCTGTC TTTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCTT CCCTCTGCAC | 716 | | |
| 246 | CCCCACCACC TCCTGCCGT CTGGCAACTG GAAAGAACAGA GTTGGCTGA TTTAACCTT | 776 | | |
| 248 | TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGAG AGAAAACCTTA | 836 | | |
| 250 | GGATACCTCT CTCACTTTCT GTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTC | 896 | | |
| 252 | TGGGTCCCCC CAAAAATCT GGTCAATTCAA GGATCCCCTC CCAAGGCTAT GCTTTCTAT | 956 | | |
| 254 | AACTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAA AAAAAA | 1012 | | |
| 257 | (2) INFORMATION FOR SEQ ID NO: 4: | | | |
| 259 | (i) SEQUENCE CHARACTERISTICS: | | | |
| 260 | (A) LENGTH: 150 amino acids | | | |
| 261 | (B) TYPE: amino acid | | | |
| 262 | (D) TOPOLOGY: linear | | | |
| 264 | (ii) MOLECULE TYPE: protein | | | |
| 266 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: | | | |
| 268 | Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala | | | |
| 269 | -23 | -20 | -15 | -10 |
| 271 | Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu | | | |
| 272 | -5 | 1 | 5 | |
| 274 | Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr | | | |
| 275 | 10 | 15 | 20 | 25 |
| 277 | Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile | | | |
| 278 | 30 | 35 | 40 | |
| 280 | Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser | | | |
| 281 | 45 | 50 | 55 | |
| 283 | Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val | | | |
| 284 | 60 | 65 | 70 | |
| 286 | Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His | | | |
| 287 | 75 | 80 | 85 | |
| 289 | Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys | | | |

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| | | | | | |
|-----|---|-----|-----|-----|-----|
| 290 | 90 | 95 | 100 | 105 | |
| 292 | Phe Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile | | | | |
| 293 | 110 | 115 | | 120 | |
| 295 | Ser Ala Asn Ser Gly Leu | | | | |
| 296 | 125 | | | | |
| 298 | (2) INFORMATION FOR SEQ ID NO: 5: | | | | |
| 300 | (i) SEQUENCE CHARACTERISTICS: | | | | |
| 301 | (A) LENGTH: 801 base pairs | | | | |
| 302 | (B) TYPE: nucleic acid | | | | |
| 303 | (C) STRANDEDNESS: single | | | | |
| 304 | (D) TOPOLOGY: linear | | | | |
| 306 | (ii) MOLECULE TYPE: cDNA | | | | |
| 309 | (ix) FEATURE: | | | | |
| 310 | (A) NAME/KEY: CDS | | | | |
| 311 | (B) LOCATION: 1..288 | | | | |
| 313 | (ix) FEATURE: | | | | |
| 314 | (A) NAME/KEY: mat_peptide | | | | |
| 315 | (B) LOCATION: 79..288 | | | | |
| 318 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: | | | | |
| 320 | ATG TGC TGT ACC AAG AGT TTG CTC CTG GCT GCT TTG ATG TCA GTG CTG | | | | 48 |
| 321 | Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu | | | | |
| 322 | -26 -25 -20 -15 | | | | |
| 324 | CTA CTC CAC CTC TGC GGC GAA TCA GAA GCA GCA AGC AAC TTT GAC TGC | | | | 96 |
| 325 | Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys | | | | |
| 326 | -10 -5 1 5 | | | | |
| 328 | TGT CTT GGA TAC ACA GAC CGT ATT CTT CAT CCT AAA TTT ATT GTG GGC | | | | 144 |
| 329 | Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly | | | | |
| 330 | 10 15 20 | | | | |
| 332 | TTC ACA CGG CAG CTG GCC AAT GAA GGC TGT GAC ATC AAT GCT ATC ATC | | | | 192 |
| 333 | Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile | | | | |
| 334 | 25 30 35 | | | | |
| 336 | TTT CAC ACA AAG AAA AAG TTG TCT GTG TGC GCA AAT CCA AAA CAG ACT | | | | 240 |
| 337 | Phe His Thr Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr | | | | |
| 338 | 40 45 50 | | | | |
| 340 | TGG GTG AAA TAT ATT GTG CGT CTC CTC AGT AAA AAA GTC AAG AAC ATG | | | | 288 |
| 341 | Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met | | | | |
| 342 | 55 60 65 70 | | | | |
| 344 | TAAGAACTGT GGCTTTCTG GAATGGAATT GGACATAGCC CAAGAACAGA AAGAACCTTG | | | | 348 |
| 346 | CTGGGGTTGG AGGTTCACT TGCACATCAT GGAGGGTTA GTGCTTATCT AATTGTGCC | | | | 408 |
| 348 | TCACTGGACT TGTCCAATTA ATGAAGTTGA TTCATATTGC ATCATAGTTT GCTTGTGTTA | | | | 468 |
| 350 | AGCATCACAT TAAAGTTAAA CTGTATTATA TGTTATTAT AGCTGTAGGT TTTCTGTGTT | | | | 528 |
| 352 | TAGCTATTATA ATACTAATTTC TCCATAAGCT ATTTGGTTT AGTCAAAGT ATAAAATTAT | | | | 588 |
| 354 | ATTTGGGGGG GAATAAGATT ATATGGACTT TTTTGCAAGC AACAGCTAT TTTTAAAAAA | | | | 648 |
| 356 | AAACTATTAA ACATTCTTT GTTTATATTG TTTTGCTCC TAAATTGTTG TAATTGCATT | | | | 708 |
| 358 | ATAAAATAAG AAAATATTA ATAAGACAAA TATTGAAAAT AAAGAAACAA AAAGTTAAAA | | | | 768 |
| 360 | AAAAAAAAA AAAAAAAA AAAAAAAA AAAA 801 | | | | |
| 363 | (2) INFORMATION FOR SEQ ID NO: 6: | | | | |
| 365 | (i) SEQUENCE CHARACTERISTICS: | | | | |
| 366 | (A) LENGTH: 96 amino acids | | | | |

VERIFICATION SUMMARY

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DATE: 02/08/2002

TIME: 08:33:00

Input Set : N:\Crf3\RULE60\10039659.txt
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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]